

EXHIBIT B

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	10	20	30	40	50	60
SEQID14	-----					
SEQID15	-----					
SEQID13	MAADGYLPDWLEDTLSEGIQWKLKPGPPPKPAERHKDDSRGLVLPGYKYLGPFNGLD					
Prim.cons.	MAADGYLPDWLEDTLSEGIQWKLKPGPPPKPAERHKDDSRGLVLPGYKYLGPFNGLD					
	70	80	90	100	110	120
SEQID14	-----					
SEQID15	-----					
SEQID13	KGEPVNEADAAALEHDKAYDRQLDSDGNPYLKYNHADAEPQERLKEDTSFGGNLGRAVFQ					
Prim.cons.	KGEPVNEADAAALEHDKAYDRQLDSDGNPYLKYNHADAEPQERLKEDTSFGGNLGRAVFQ					
	130	140	150	160	170	180
SEQID14	-----MAPGKKRPVEHSPVEPDSSSGTGKAGQQPARKRLNFGQTGDAD					
SEQID15	-----					
SEQID13	AKKRVLEPLGLVEEPVK2APGKKRPVEHSPVEPDSSSGTGKAGQQPARKRLNFGQTGDAD					
Prim.cons.	AKKRVLEPLGLVEEPVK2APGKKRPVEHSPVEPDSSSGTGKAGQQPARKRLNFGQTGDAD					
	190	200	210	220	230	240
SEQID14	SVPDPQLGQPPAAPSGLGTNTMATGSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVI					
SEQID15	-----MATGSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVI					
SEQID13	SVPDPQLGQPPAAPSGLGTNTMATGSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVI					
Prim.cons.	SVPDPQLGQPPAAPSGLGTNTMATGSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVI					
	250	260	270	280	290	300
SEQID14	TTSTRTWALPTYNNHLYKQISSQSGASNDNHYPGYSTPWGYFDNRFHCHFSPRDWQRLI					
SEQID15	TTSTRTWALPTYNNHLYKQISSQSGASNDNHYPGYSTPWGYFDNRFHCHFSPRDWQRLI					
SEQID13	TTSTRTWALPTYNNHLYKQISSQSGASNDNHYPGYSTPWGYFDNRFHCHFSPRDWQRLI					
Prim.cons.	TTSTRTWALPTYNNHLYKQISSQSGASNDNHYPGYSTPWGYFDNRFHCHFSPRDWQRLI					
	310	320	330	340	350	360
SEQID14	NNNWGFRPKRLNFKLFNIQVKEVTQNDGTTTIANHLTSTVQVFTDSEYQLPYVLGSAHQG					
SEQID15	NNNWGFRPKRLNFKLFNIQVKEVTQNDGTTTIANHLTSTVQVFTDSEYQLPYVLGSAHQG					
SEQID13	NNNWGFRPKRLNFKLFNIQVKEVTQNDGTTTIANHLTSTVQVFTDSEYQLPYVLGSAHQG					
Prim.cons.	NNNWGFRPKRLNFKLFNIQVKEVTQNDGTTTIANHLTSTVQVFTDSEYQLPYVLGSAHQG					
	370	380	390	400	410	420
SEQID14	CLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPPSMLRTGNNFTFSYTFEDVFP					
SEQID15	CLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPPSMLRTGNNFTFSYTFEDVFP					
SEQID13	CLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPPSMLRTGNNFTFSYTFEDVFP					
Prim.cons.	CLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPPSMLRTGNNFTFSYTFEDVFP					

	430	440	450	460	470	480
SEQID14	HSSYAH	SQSLDR	LMNPLID	QYLYLS	RNTNPS	GGTTTQ
SEQID15	HSSYAH	SQSLDR	LMNPLID	QYLYLS	RNTNPS	GGTTTQ
SEQID13	HSSYAH	SQSLDR	LMNPLID	QYLYLS	RNTNPS	GGTTTQ
Prim.cons.	HSSYAH	SQSLDR	LMNPLID	QYLYLS	RNTNPS	GGTTTQ
	490	500	510	520	530	540
SEQID14	PCYRQQR	VSKTSAD	NNNSEY	SWTGAT	KYHLNG	RDSL
SEQID15	PCYRQQR	VSKTSAD	NNNSEY	SWTGAT	KYHLNG	RDSL
SEQID13	PCYRQQR	VSKTSAD	NNNSEY	SWTGAT	KYHLNG	RDSL
Prim.cons.	PCYRQQR	VSKTSAD	NNNSEY	SWTGAT	KYHLNG	RDSL
	550	560	570	580	590	600
SEQID14	IFGKQGS	EKTNDI	EKVMIT	DEEEIR	TNPNV	ATEQYGS
SEQID15	IFGKQGS	EKTNDI	EKVMIT	DEEEIR	TNPNV	ATEQYGS
SEQID13	IFGKQGS	EKTNDI	EKVMIT	DEEEIR	TNPNV	ATEQYGS
Prim.cons.	IFGKQGS	EKTNDI	EKVMIT	DEEEIR	TNPNV	ATEQYGS
	610	620	630	640	650	660
SEQID14	LPGMVWQ	DRDVYL	QGPIWAKI	PHTDGH	FHPSP	LMGGFGL
SEQID15	LPGMVWQ	DRDVYL	QGPIWAKI	PHTDGH	FHPSP	LMGGFGL
SEQID13	LPGMVWQ	DRDVYL	QGPIWAKI	PHTDGH	FHPSP	LMGGFGL
Prim.cons.	LPGMVWQ	DRDVYL	QGPIWAKI	PHTDGH	FHPSP	LMGGFGL
	670	680	690	700	710	720
SEQID14	FSAAKFAS	FITQYST	GQVSVEI	EWELQ	KENSKR	WNPEIQ
SEQID15	FSAAKFAS	FITQYST	GQVSVEI	EWELQ	KENSKR	WNPEIQ
SEQID13	FSAAKFAS	FITQYST	GQVSVEI	EWELQ	KENSKR	WNPEIQ
Prim.cons.	FSAAKFAS	FITQYST	GQVSVEI	EWELQ	KENSKR	WNPEIQ
	730					
SEQID14	SEPRPIG	TRYLTRNL				
SEQID15	SEPRPIG	TRYLTRNL				
SEQID13	SEPRPIG	TRYLTRNL				
Prim.cons.	SEPRPIG	TRYLTRNL				

Alignment data :

Alignment length : 735

Identity (*) : 533 is 72.52 %

Strongly similar (:): 0 is 0.00 %

Weakly similar (.) : 0 is 0.00 %

Different : 202 is 27.48 %

Sequence 0001 : SEQID14 (598 residues). VP2

Sequence 0002 : SEQID15 (533 residues). VP3

Sequence 0003 : SEQID13 (735 residues). VP1

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